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Title:
Perfect score:
Sequence:
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Maximum
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No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein -
     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB seq
    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein search, using sw model
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length: 2000000000
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2393
1 MPILSLCTICSDFFDHSRDV.....VRIKTVSSASQPKLDTFLCQ 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
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                         Length
   GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd
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  MYHA BOVIN
G160 MOUSE
MYSC_CHICK
MYSL_DICDI
MYH3_RAT
MYH3_HUMAN
MYS_BEGIR
MYSL_CABEIL
MYHA_HUMAN
MYS_CABEIL
MYHA_HUMAN
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MYSA_CABEIL
MYHA_HUMAN
MYSA_CABEIL
MYHA_HUMAN
RA50_THEVO
MYH9_HUMAN
RA50_THEVO
MYH9_HUMAN
RA50_THEVO
MYH9_HUMAN
YL17_CABEIL
MYH4_HUMAN
TMF1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105224
099323 drosophila
p29616 gallus gall
p12847 rattus norv
p0879 dictyosteli
p11055 homo sapien
p24733 aequipecten
099105 oryctolagus
09ukx3 homo sapien
p12844 caenorhabdi
p35580 homo sapien
p25386 saccharomyc
010411 schizosacch
p25386 saccharomyc
010411 schizosacch
p3557 homo sapien
p58302 thermoplasm
p05659 acanthamoeb
p02562 oryctolagus
p10567 caenorhabdi
062812 rattus norv
p50533 xenopus lae
p13535 homo sapien
01102 caenorhabdi
09y623 homo sapien
011012 homo sapien
01102 caenorhabdi
09y623 homo sapien
01102 homo sapien
01102 caenorhabdi
09y623 homo sapien
01102 denorihabdi
090298 caenorhabdi
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090298 caenorhabdi
090399 cyprinus ca
p14105 gallus gall
075665 homo sapien
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165.5	165.5	166	166	167.5	167.5	167.5	167.5	168	168	168.5	168.5
6.9	6.9	6.9	6.9	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0
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MYSP_DIRIM	G160_HUMAN	MYHB_MOUSE	MYSD_CAEEL	AKA9_HUMAN	MYHB_CHICK	MYSB_CAEEL	MFP1_ARATH	MYHB_RABIT	MFP1_LYCES	TPR_HUMAN	MYH2_HUMAN
P13392 dirofilaria		O08638 mus musculu	P02567 caenorhabdi	Q99996 h a-kinase	P10587 gallus gall	P02566 caenorhabdi	Q91w85 arabidopsis	P35748 oryctolagus	P93203 lycopersico	homo	Q9ukx2 homo sapien

## ALIGNMENTS

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Myos Spec myos	InterPro; IPRO04009; Myosin_N.	P08799; 1LVK.	23; BAA36494.1; -	to license@	requires a license agreement (See http://www.is	ong as its con oved. Usage b	European Bioinformatics Institute. There are no restrictions on if	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Biginformatics and the FMRI outstation.	- SIMILARITY: CONTAINS 1 IQ DOMAIN.	7	CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,		CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2	N THAT CONSISTS OF 2 HEA	CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND	-!- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,	osin heavy chain II-B.";	<pre>Itoh K., Adelstein R.S.; "Neuronal cell expression of inserted isoforms of vertebrate nonmuscle</pre>	NO F	SEQUENCE OF 204-302 FROM N.A.		us nonmuscle myosin hea	SEQUENCE FROM N.A. Ohara M., Ishiquro N., Shinagawa M.;	[1]	Bovinae; Bos.	<pre>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;</pre>	(Bovine).	muscle myosin heavy chain-B) (NMMHC-B).	Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain,	(Rel. 40, Last	\(\lambda 2 \) 991; 16-OCT-2001 (Rel. 40, Created)		LT 1 BOVIN

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RESULT
G160_MG
G160_MC
G1 O1
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DT 115
DT 15
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GN GG
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OC EL
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Best Local
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Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR0193; MYOSINHEAVY.
ProDom; PD000355; Myosin_head; 1
SMART; SM00015; IQ; 1.
SMART; SM000142; MYSC; 1.
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MOD_RES
MOD_RES
SEQUENCE
                                      Golgin-160 (Male-enhanced antigen-2) (MEA-2). GOLGA3 OR MEA2.
                                                                 G160_MOUSE STANDARD; PRT; 1325 AA p55937; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update)
Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria;
                                                                                                                                        MOUSE
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DOMAIN
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PROSITE: PS50096; IQ; 1.

Myosin; ATP-binding; Calmodulin-binding; Actin-binding; Multigene family.

Coiled coil; Alkylation; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                           ITSLRKKSDDPPGNLEPASATNETVSRLVFESPAPVEMMNPRLHQPPFG-DEIDLNTTFD::::||:::||:::
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COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
MW; 6144354451C0F790 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 198;
Pred. No. 0.
Craniata; Vertebrata; E
Sciurognathi; Muridae;
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            Euteleostomi;
  Murinae;
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Matches 94
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1 TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. TRANSCRIPTS CAN FOUND IN SPERMATIOS DURING SPERMATOGENESIS. NO EXPRESSION IN LETTING CELLS, SPERMATOGONIA, OR SPERMATOCTIES.

1 SIMILARITY: HIGH, TO HUMAN GOLGIN-160.

1 CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-19 OR MET-30 IS THE TAYBUT OF THE TAYBUT
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DOMAIN 201 204 POLY-ALA.

SEQUENCE 1325 AA; 149880 MW; 3230636962C687B0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:96958; Golga3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kondo M., Sutou S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLAQEEENVLDA-EFLKNE-----LDSVKAQLSQKDREKR-----DSQAIIDTLRD 109
                                                                                      HKVSKPESQLSLGGQRCVGELDEELAGAFPLFIRNAVLGQKQPNRTTAESRSSTDVVRI 416
                                                                                                                                                                                                                                                               HOPPFGDEIDLNTT
                                                                                                                                                                                                                                                                                                                                                                                                                                         KLELRSAQKDLQSADQEITSLRKKSDDPPGNLEPASATNETVSRLVFESPAPVEMMNPRL 306
                                                                                                                                                                                                                                                                                                                                                      QKEMKTKHKAYENA---VSILSRRLQEA---LASKEATDAELNQLRAQSTG--GSSDPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLAVKSNQVEHLQQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLEERNATVESLQNALNKAEMLCSTLKKOM-----KFLEQ-----RODET-----KQ 151
    KRLEESNKKLAL - - - - - -
                                                                                                                                                                             HEKIRALEVELQNVGQSKILLEKELQEVITMTSQELEESREKVLELEDELQESRGFRRKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDEMETHLOSLKFDKEQMIALTEANETLKKQTEELQQEAKKAITEQKQKMKRLGSDLTSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKATKKRLDSEMKELRQELIKLQGEKKTVEVEHSRLQKDMSLVHQQMAELEGHLQSVQKE 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AREEAHRLKCKMKTMEQIELLLQSQRSEVE----EMIRDMGVGQSAVEQLAVYCVSLKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TATLRKQMQKVKEQFVQQKVMVEAYRRDATSKDQLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.0%; Score 192.5; DB 1;
22.4%; Pred. No. 0.012;
tive 80; Mismatches 156;
                                                                                                                                                                                                                                                               -----FDVNTPPTQTSGS-QHCLPKKLCLERARSPMQNVLKKV 357
ELEHERGKLTGLGQSNAALREHNSILETALAKREADLVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --LKEA----RKATGELADRLKKDLVSSRSKLKTLNTELDQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSCRIPTS CAN
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ne Golgi
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                                                                                                                                                                                                                                                                                                                                                      874
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RESULT 3
MYSN\_DROME
ID MYSN\_D
AC Q99323

MYSN\_DROME Q99323;

STANDARD;

PRT;

2017 A

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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994
01-JUN-1994
16-OCT-2001
                                                                                                                        DOMAIN
DOMAIN
                                                              VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                          Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tall; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A36014; A36014.
PIR; B36014; B36014.
HSSP; P08799; IMMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myosin
ZIP.
                                                                                                                                                              DOMAIN
                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                        PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head; SMART; SM00015; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ketchum A.S., Stewart C.T., Stewart M., Kiehart D.P.; "Complete sequence of the Drosophila nonmuscle myosin't transcript: conserved sequences in the myosin tail and splicing in the 5' untranslated sequence."; Proc. Natl. Acad. Sci. U.S.A. 87:6316-6320(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO04009; Myosin_N.
InterPro; IPRO02928; Myosin_tail.
InterPro; IPRO01609; Myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0005634; zip. InterPro; IPR000048; IQ.
                                                                                                   DOMAIN
                                                                                                               DOMAIN
                                                                                                                                                                            NP_BIND
                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                         ATP-binding;
                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-90349606; PubMed-2117279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: NONMUSCLE MYOSIN APPEARS TO BE RESPONSIBLE FOR CELLULARIZATION. REQUIRED FOR MORPHOGENESIS AND CYTOKINESIS. ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LOUGH CORM (SHOWN HERE) A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               M35012; AAA28713.1;
                                                                                                                                                                                                                                                               SM00242; MYSC;
  88; Conser
                                                                                                                                                                                                                                        Alternative
                                                                                                                                                                                                                                                  PS50096; IQ;
                                                                                     830
886
225
250
250
682
705
742
1303
1303
1303
                                                                                                                                                                                                                   Calmodulin-L'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel.
(Rel.
(Rel.
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophilidae; Drosophila.
                                                              ΑĄ.
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29,
                                                                                                 829
859
2017
232
260
694
727
758
2017
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0, Last annotation update)
non-muscle (Zipper protein) (Myosin
           7.9%;
23.8%;
                                                              232016
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Last
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 61;
 Score 190; DB
Pred. No. 0.02
61; Mismatches
                                                              W.
                                                                                                                    ATP.
25 KDA/50 KDA JUNCTION.
50 KDA/20 KDA JUNCTION.
ACTIN-BINDING.
REACTIVE SULFHYDRYL/ACTIN-BINDING
                                                            GLOBULAR TAILPIECE.
MISSING (IN SHORT ISOFORM)
W; 73E3CB02BA8F2528 CRC64
                                                                                              ALPHA-HELICAL TAILPIECE
                                                                                                                                                                                  IQ. COILED COIL (POTENTIAL)
                                                                                                                                                                                                              MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                     Coiled coil; Actin-binding;
            DB 1;
.025;
  145;
                        Length 2017;
 Indels
                                                              CRC64
                                                                                                 (LMM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restricti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heavy-chain
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 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outstation
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Gaps
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RESULT 4
MYSC_CHICK
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Biol. Chem. Hoppe-Seyler: , , 1810. Chem. Hoppe-Seyler: , , 1910. Chem. Hoppe-Seyler: , , 1910. Chem. Hoppe-Seyler: ATTION: MUSCLE CONTRACTION.  
-!- FUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2  
-!- SUBUNITS: (MHC) , 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)  
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).  
-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils:  
-!- TISSUE SPECIFICITY: VENTRICULAR MUSCLE AND TRACES LEVELS IN THE  
ATRIUM. ALSO TRANSIENT EXPRESSION IN SKELETAL MUSCLE DURING FETAL  
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING  
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,  
-!- MISCELLANEOUS: EACH MYOSIN HERVY CHAIN CAN BE SPLIT INTO 1 LIGHT  
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE  
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ol-APR-1993 (Rel. 25, Created)
Ol-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Myosin heavy chain, cardiac muscle isoform
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYSC_CHICK P29616;
                                                                                                                                                                                                                                                                                                                                                                             myosin heavy chain
J. Mol. Evol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; e
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1592 N--EELEDDL 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 65-1102 FROM N.A.
STRAIN-BROILER BREEDERS; TISSUE-Heart;
MEDLINE-92130260; PubMed-1774788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1432
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                                                                                                                                                                                                            + +
                                                                                                                                                                                                                                                         "Amino-acid sequence of cardiac muscle myosin."
                                                                                                                                                                                                                                                                                            Watanabe B.;
                                                                                                                                                                                                                                                                                                                                                                                                       Jakovcic S., Zak R.;
"Structural and phylogenetic analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                              Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                                             Biol.
                                                                                                                                                                                                                                                                                                           MEDLINE=93039740;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLGLSSKLRQIESEKEALQEQLEEDDEAKRNY---ERKLAEVTTQMQEIKKKAEEDADLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RCVGELDEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKSDDPPGNLEPASATNETVSRLVFESPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---LKCKMKTMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDTLRDTLEER----NATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHR-
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                                                                                                                                                                                                                                                                                                                                            OF 1-259.
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                                                                                                                                                                                                                                                                                                           PubMed=1418675;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasian:
                                                                                                                                                                                                                                                                           the short subfragment-2
                                                                                                                                                                                                                                                                                                                                                                                                                                          В.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ion update)
isoform (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                             of the
                                                                                                                                                                                                                                                                                                                                                                                                                                          Perlman D., Gupta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                             chicken ventricular
                                                                                                                                                                                                                                                                            in
                                                                                                                                                                                                                                                                            adult
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idae; Phasianinae;
                                                                                                                                                                                                                                                                            chicken
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01-OCT-1989
01-OCT-1989
16-OCT-2001
                           Myosin
MYH3.
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Myosin; Muscle protein; Coiled coil;
ATP-binding; Multigene family.
 Eukaryota;
               Rattus norvegicus
                                                                                                             MYH3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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SIMILARITY: THE |
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(Rel. 40,
 Metazoa;
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                                         chain,
                                                                                                             STANDARD;
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              (Rat)
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                                        fast
 Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.8%;
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                                                      Last sequence update)
Last annotation updat
                                                                                  Created)
                                         skeletal muscle, embryonic
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V -> A (IN REF. 1).
CS -> FAL (IN REF. 1).
H -> Q (IN REF. 1).
T -> R (IN REF. 1).
MW; 2293668D049825DC CR
                                                                                                                                                                                 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 185.5; DB 1; Pred. No. 0.022; 2; Mismatches 167;
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 Craniata; Vertebrata; Euteleostomi;
                                                                                                            PRT;
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                                                                                                             1940 AA
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                                                      update)
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54 GKKTIINKLFFDLAQEEENV-LDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLE 112

Query Match Best Local S Matches 74

74; Conserv

Conservative

7.8%;

Score 185.5; DB 1; Pred. No. 0.041; 4; Mismatches 180;

Indels Length 1940;

41;

Gaps

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J. MOI. BIOI. 190:291-317(1986).

C. --- SUBGUNIT: MUSCLE CONTRACTION.

C. --- SUBGUNIT: MUSCLE WOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

C. --- SUBGUNIT: MUSCLE WOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

C. --- SUBGUNIT: MUSCLE WOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

C. --- SUBGUNIT: CHAIN SUBUNITS (MLC-2).

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

C. --- SUBGELLULAR LOCATION: Thick filaments of the myofibrils.

C. --- SUBGELLULAR LOCATION: Thick filaments of the myofibrils.

C. --- CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

C. CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

C. CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

C. --- FYM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY

ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

ALKYLATED AND ARE REQUIRED FOR MYOSIN CHAMD. IT CAN LATER BE

SELIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                             Pfam; PF00612; IQ; 2. Pfam; PF00063; myosin_head; 1. Pfam; PF02736; myosin_N; 1. Pfam; PF02736; myosin_tail; 1. Pfam; PF01576; myosin_tail; 1. PRINTS; PR00193; MYOSINHEAVY. PF0D0m; PD000355; myosin_head; 1
                                                                          NP_BIND
DOMAIN
DOMAIN
           MOD_RES
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete nucleotide and encoded amino acid sequence of a mammalian myosin heavy chain gene. Evidence against intron-dependent evolution of the rod.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X04267; CAA27817.1;
PIR; A24922; A24922.
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                         DOMAIN
                                                                                                                                                                       Multigene
                                                                                                                                                                                                       Myosin;
                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002928;
InterPro; IPR002017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed.
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                                                                                                                                           DOMAIN
                                                                                                                                                         DOMAIN
                                                                                                                                                                                     Calmodulin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strehler E.E., Strehler-Page M.-A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way find and the first transitions as long as its content.
                                                                                                                                                                                                                      SM00242; MYSC;
E; PS50096; IQ;
                                                                                                                                                                                                                                                   SM00015; IQ;
                                                                                                                                                                                                       Muscle protein;
                                                                                                                                                                       family.
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                                                                                                                                                                                                                                                                                                                                                                                            Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                               Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                              Myosin_N
                                                                                                                                                                                                       Coiled coil; Thick filament; Actin-binding,
              WW.
                                                                        IQ.

COILED COIL (POTE ATP (POTENTIAL).

ACTIN-BINDING.

ACTIN-BINDING.
           METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
M; B5D546A596E5A696 CRC64;
                                                                                                                                                       MISOYM
                                                                                                                                                         HEAD-LIKE
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or send a
                                                                                                                                                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain; Yam J.W.P., Chan K.W., Hsiao W.L.W.;
"Suppression of transformed phenotype by overexpression of nonmuscle myosin heavy chain-B in p53vall35-transformed rat fibroblast.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS, CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9JLTO;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin heavy chain, nonmuscle type B (Cellular type B) (Nonmuscle myosin heavy chain-B) (NMMHC MYH10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAT
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                               EMBL; AF139055; AAF61445.1; -. InterPro; IPR000048; IQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYHA_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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                                                                                                                                                                                          CAPPING.

CAPPING:
SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC CHAIN SUBUNITS (MLC-2).

REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE.

CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPT CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                        European Bioinformatics Institute. They by non-profit institutions as long a filed and this statement is not removed.
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                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                   requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                  IPR000048;
IPR004009;
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              Myosin_N
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(NMMHC-B).
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SMART; SM00242; MYSC;
PROSITE; PS50096; IQ;
                                                           "Conserved protein domains in a myosin Dictyostelium discoideum.";
                                                                                                                                                  Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida;
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InterPro; IPR001609; myosin_
Pfam; PF00063; myosin_head;
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MEDLINE=90353583; PubMed=2387408;
             STRAIN-AX2
                                                                                     Warrick H.M., de Lozanne A., Leinwand L.A.,
                                                                                                  SEQUENCE FROM N.A. MEDLINE=87092266;
                                                                                                                                       NCBI_TaxID=44689;
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I heavy chain, non musc
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ATP (POTENTIAL).

ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

BLKYLATION (SH-2) (POTENTIAL).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation

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Smith C.A., Rayment I.; "X-ray structure of the magnesium(II).ADP.vanadate complex of the "X-ray structure of the magnesium otor domain to 1.9-A resolution."; Biochemistry 35:5404-5417(1996).
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                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
MEDLINE-98070605; PubMed-9405148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "X-ray structures of the myosin motor discoideum complexed with MgADP.BeFx Biochemistry 34:8960-8972(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
MEDLINE=95345066; PubMed=7619795;
Fisher A.J., Smith C.A., Thoden J.B.,
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MEDLINE-97452580; PubMed-9305951;
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Gerisch G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Replacement of threonine
                                                                                                                                                                                                                                                                                                                                                     lick A.M., Bauer C.B., Thoden J.B., Rayment I.;
-ray structures of the MgAPP, MgATPgammaS, and MgAMP
the Dictyostelium discoideum myosin motor domain.";
ochemistry 36:11619-11628(1997).
                             PTM: PHOSPHORYLATION INHIBITS THICK FILAMENT THE ACTIN-ACTIVATED ATPASE ACTIVITY.
MISCELLANEOUS: DICTYOSTELIUM MYOSIN II HAS NO ACTIVITY. PERHAPS CORRELATED WITH THE ABSENCE POSITION (688).
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SIMILARITY:
                                                                                     DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
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                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF02736; Myosin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                    1059
                                                           1005
                                                                                                                                                                                                                                                                                                                                                                                     Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR001609; myosin_he
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                 NP_BIND
                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                  Myosin;
                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00193; MYOSINHEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DictyDb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                         912
 355
                                        295
                                                                              235
                                                                                                 954
                                                                                                                     176
                                                                                                                                                            116
                                                                                                                                                                                852
                                                                                                                                                                                                 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A26655;
S00250;
1MMA; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1MMD;
1MMG;
 KKVHKVSKPESQLSLGGQRCVGELDEE
                   A----ANKKLQ---
                                                                                                --EELEEMKR-VNDGQSDTISRLEKIKDELQKEVEELTES----FSEESKDKGVLEKT
                                                                                                                                         LALENLQNQKRSVE----
                                                                                                                                                          ATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQS
                                                                                                                                                                              DKLEKSLKDTESNVLDLQRQLKAEKETLKAMYDSKDALEAQKRELEIRVEDMESELDEKK
                                                                                                                                                                                                NKLFFDLAQEEENVLDAE-FLKNELDSVKAQLSQKD---REKRDSQAIIDTLRDTLEERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1MND;
                                      SPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPKKLCLERARSPMQNVL
                                                           RVR
                                                                             KLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKKSDDPPGNLEPASATNETVSRLVFE
                                                                                                                   QRSEVEEMIRDMGVGQS-AVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1MMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1MNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M14628;
                                                                                                                                                                                                                     82;
                                                                                                                                                                                                                                                                                                                                                                                                                    SM00242; MYSc;
                                                                                                                                                                                                                                                                                                                                                                                                                              SM00015; IQ;
                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PD000355; myosin_head;
                                                           LQSELDDLTVRLDSETKD----KSELLRQKKKLEEELKQVQEALAA
                                                                                                                                                                                                                                                                                 J; 1.

J; 1.

Actin-bing...

J; Methylation; A

761 MYOS

791 IQ

2116 CC

/9 1186 A

130 660

738 752

130 130

678 678

1823

1823

1823

1823

1823
                                                                                                                                                                                                                                                                                                                                                                                                          PS50096; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DD01008; mhcA
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17-AUG-96.
03-DEC-97.
03-DEC-97.
17-AUG-96.
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678
1823
1833
2029
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                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S00250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA33227.1;
                                                                                                                                                                                                                                                                     ĄΑ;
                                                                                                                                                                                                                                                                              2029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myosin_head.
                                                                                                                                                                                                                               25
                                                                                                                                                                                                                                                                                                                                                                                                Actin-binding;
                                                                                                                                                                                                                                                                    243871
                    -GEYTELNEKF --
                                                                                                                                                                                                                             . 18;
                                                                                                                                       EKVRDLEEELQEEQKLRNTLEKLKKKYE--
                                                                                                                                                                                                                     60;
                                                                                                                                                                                                                                                                     Ψ¥
                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                             PHOSPHORYLATION PHOSPHORYLATION PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                          IQ.
COILED
                                                                                                                                                                                                                                                                                                          METHYLATION (DI-)
ALKYLATION (SH-1)
                                                                                                                                                                                                                                                                                                                              ACTIN-BINDING
ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                              MYOSIN
                                                                                                                                                                                                                     Mismatches
 381
                                                                                                                                                                                                                                                                                                                                                                                        ng; ATP-binding;
Alkylation; Pho:
                                                                                                                                                                                                                                                                     2FC3770BB1EE56A1
                    NSEVTARSN-
                                                                                                                                                                                                                              No. 0.045;
                                                                                                                                                                                                                                                                                                                                                          COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                              HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no rest
                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                     108;
                                                                                                                                                                                                                                                                   (BY MHCK).
(BY MHCK).
EE56A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
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                                                                                                                                                                                                                                                                                                  BY MHCK)
                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                 3D-structure;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                      Length
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                                                          -ETAAKLAQE
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                                                                                                1004
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В

1097

VAVN---

-NELDEE

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MYH3 HUMAN STANDON....
MYH3 HUMAN STANDON...
P11055; Q15492;
O1-JUL-1989 (Rel. 11, Created)
O1-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat)
16-OCT-2001 (Rel. 40, Last skeletal muscle, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myosin heavy myosin heavy MYH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eller M.S., Stedman H.H., Sylvester J.E., Rubinstein N.A., Kelly A.M., Sarkar S.; "Nucleotide sequence of full length human chain cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYH3.
Homo sapiens (Human).
Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myosin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eller M.S., Stedman H.H., Sylvester J.E., Raychowdhury M.K., Rubinstein N.A., Kelly "Human embryonic myosin heavy chain cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                           "Expression and DNA sequence analysis muscle myosin heavy chain gene.";
Nucleic Acids Res. 17:6167-6179(1989).
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89366648;
Karsch-Mizrachi I
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 856-1940 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bober E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE Skeletal muscle;
MEDLINE 90235862; PubMed 1691980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 856-1940 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conservation of the myosin rod, chromosomal locus and specific transcription of the gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90033298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 774-1940 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=89263803; PubMed=2726495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAMOH
                                                                                                         DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDE: CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                SUBUNIT: MUSCLE WOOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MAC), 2 ALKALI LIGHT CHAIN SUBUNITS (MC-2).

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

DEVELOPMENTAL STAGE: ABUNDANTLY PRESENT IN FETAL SKELETAL MU AND NOT PRESENT OR BARELY DETECTABLE IN HEART AND ADULT SKEL
                                                            SIMILARITY: CONTAINS 1 MYOSIN-LIKE SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                              SUBFRAGMENT (S2)
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acids Res. 17:3591-3592(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchberger-Seidl A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256:21-28(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cha:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189:55-65(1990).
                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=2771643;
., Travis M., Blau H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=2806546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  developmentally controlled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Braun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T.
                                                                                                                                                                                                                                                                                                                                                                                        ., Leinwand
of a human
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                                                                            GLOBULAR
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Interspecies s
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                                                                            HEAD
                                                                                                                                                                                                                                                                                                                                                                                        embryonic skeletal
                                                                                                                                                                                                                                                                                                                                                                                                         L.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isoforms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myosin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Muscle
                                                                            DOMAIN
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Best Local
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CONFLICT
SEQUENCE
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pfam; pF02736; Myosin_n; 1.
pfam; pF01576; Myosin_tail; 1.
pRINTS; pR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X13988; CAA32167.1; -. EMBL; X13100; CAA31492.1; -. EMBL; X51593; CAA35942.1; -. EMBL; X15696; CAA33731.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002928;
InterPro; IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a
 398
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                                                                                                                                                                     173
                                                                                   281
                                                                                                                           221
                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                              GKKTIINKLFFDLAQEEENV-LDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; P08799; 1MMD
160720; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S04090;
                   DIQLALEEAEAALEHEEAKILRIQLELTQVKSEIDRKIAEKDEEIEQLKRNYQRTV---E
                                                                                                                                                                                                                                GKNEEIQRSLSELTTQKSRLQTEAGELSRQLEEKESIVSQLSRSKQAFTQQTEELKRQLE 1321
 KQPNRTTAESRSSTDVVRI 416
                                                             VKRENKNLEQEIADLTEQIAENGKTIHE:
                                                                               ASATNETVSRLVFESPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPK-
                                                                                                      LAAALDKKQRNFDKVLAEWKTKCEESQAELEASLKESRSLSTELFKLKNAYEEALDQLET
                                                                                                                          LADRLKKDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKKSDDPPGNLEP
                                                                                                                                              QRTEELEEAKKKLAQRLQD----SEEQVEAVNAKCASLEKTKQRLQGEVEDLMVDVERANS
                                                                                                                                                                                        EENKAKNALAHALQSSRHDCDLLREQYEEEQEGKAELQRALSKANSEVAQWRTKYETDAI
                                                                                                                                                                                                           ERNATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00242; MYSc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00015; IQ;
                                s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muscle protein;
                                                                                                                                                                  -LQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKK-----EYENLKEARKATGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR004009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000048;
                                                                                                                                                                                                                                                                                                                              1331
1391
1608
1663
1940
                                                                                                                                                                                                                                                                                                                                                                                840
179
656
758
130
696
706
                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                             ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQ;
                                                                                                                                                                                                                                                                                                                                      781
811
1933
186
678
772
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706
1331
1332
1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQ.
Myosin_N.
Myosin_tail.
myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding;
                                                                                                                                                                                                                                                                                    7.7%;
19.5%;
                                                                                                                                                                                                                                                                                                                             224035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coiled coil; Thick filament;
                                                                                                                                                                                                                                                                           85;
                                                                                                                                                                                                                                                                                                                              ¥,
                                                                                                                                                                                                                                                                                   Score 184.5; DE Pred. No. 0.046;
                                                                                                                                                                                                                                                                                                                            KK -> QE (IN REF. 1 A
SR -> RA (IN REF. 3).
RG -> QT (IN REF. 2).
MW; 43CA58C6A4BA1253
                                                                                                                                                                                                                                                                                                                                                                    ALKYLATION (SH-2
A -> G (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                          ALKYLATION (SH-1
                                                                                                                                                                                                                                                                                                                                                                                                    METHYLATION (TRI-)
                                                                                                                                                                                                                                                                                                                                                                                                              ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                  COILED COIL (POT ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NISOYM
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                            COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEAD-LIKE
                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                          179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                           AND
                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                             CRC64;
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AC P24733;

DT 01-MAR-1992 (
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                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Adductor muscle;
MEDLINE-91088319; PubMed=2263488;
Nyitray L., Goodwin E.B., Szent-Gyorgyi
"Nucleotide sequence of full length cDNA
muscle myosin heavy chain.";
Nucleic Acids Res. 18:7158-7158(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Adductor muscle;
MEDLINE-92011595; PubMed=1917970;
Myitray L., Goodwin E.B., Szent-Gyoergyi A.G.;
"Complete primary structure of a scallop striated muscle myosin heavy chain. Sequence comparison with other heavy chains reveals regions that might be critical for regulation.";
J. Biol. Chem. 266:18469-18478(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence upda
16-OCT-2001 (Rel. 40, Last annotation up
Myosin heavy chain, striated muscle.
Aequipecten irradians (Bay scallop).
Eukaryota, Metazoa; Mollusca; Bivalvia;
Pectinoidea; Pectinidae; Argopecten.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resolution: implications for Structure 4:21-32(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure of the regulatory domain of scallop myosin resolution: implications for regulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houdusse A., Cohen C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96419133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:306-312(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure of the regulatory domain of scallop myosin resolution ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Szent-Gyorgyi A.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS)
MEDLINE-94173332; PubMed-8127365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=31199;
                                                            L; X55714; CAA39247.1;

$13557; $13557.

$440997; A40997; A40997;

$1SCM; 30-APR-94.

$1WDC; 11-JUL-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: MUSCLE CONTRACTION.

FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAP EURCTION: MYOSIN IS A PROTEIN THAT ENDINGTY THAT IS A CTIVATED BY F-ACTIN.

SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSI:
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNIT:
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-3).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harrison D.H., Schlichting I., yorgyi A.G., Cohen C.;
      IPR000048;
IPR004009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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   Myosin_N
                                 Į,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (2.0 ANGSTROMS) OF 777-836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pteriomorphia; Pectinoida;
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MYSU\_RABIT Q99105; Q1-JUN-1994 Q1-JUN-1994 15-JUL-1998

(Rel. (Rel.

29, Created)29, Last sequence update)36, Last annotation update)

Myosin

heavy

chain,

embryonic smooth muscle isoform (Fragment).

MYSU\_RABIT

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SEQUENCE
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Pfam; PF00063; myosin_head;
Pfam; PF02736; Myosin_tail;
Pfam; PF01576; Myosin_tail;
PRINTS; PR00193; MYOSINHEAVY
                                                                                                                    1196
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ATP-binding;
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                                                                                                                                                                                                                                                                                           QDKAHKDNQ--ISTLQGEISQQDEHIGKLNKEKKALEEANKKTSDSLQAEEDKCNHLNK-
                                                                                               HCLPKKLCLERARSPMQNVLKKVHKVSKPESQLS-----LGGQRCVGELDEELAGAFPL
                                                                                                                                      PGNLEPASATNETVSRLVFESPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQ
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Alkylation;
                                QSQKSRLQAENSDLT
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                                                     411
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Pred. No. 0.
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(SH-2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tities requires a license agreement (See http://www.isb-sib.ch/announce, send an email to license@isb-sib.ch).
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BIOL CHEM. 266:3768-3773(1991).

FUNCTION: MUSCLE CONTRACTION.

SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

SUBCELLANGE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CYCLES OF A 28-RESIDUE REPEAT PATTERN CONFOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

MISCELLANBOUS: BACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBFRAGMENT (S2).
SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONSERVED.
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                                                                                                                                                                                                                            DLKDLEAQIEAANK----ARERRVKQLRRLQAQMKDYQRELEEARGSRDEIFAQSKE----
                                                                                                                                                                                                                                                                                                                                                                                                 AEMLCSTLKKQMKFLEQRQDE-----TKQAREEAHRLKCKMK-----TMEQIEL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QNKQLRADMEDLMSSKDDVGKNVHELEKSKRALEQQVEEMRTQLEELEDELQATEDAKLR
EARMRQLEEELEEEQSNMELLNDRFRK----
                                                                                                            SEKKLKSLEAEILQLQEELASSERARRHAEQERDEL---ADEIANSASGKSALLDEKRRL
                                                                                                                                                                  SRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKKSDDPPGNLEPASATNETVSRL
                                                                                                                                                                                                                                                                               LLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVS
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                                                   ----VFESPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           501 AA;
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22.0%;
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COILED COIL (POTENTIAL).
; 49F793247D00973E CRC64;
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TTLQVDTLNAELAAERSAAQKSD
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Pfam;

PF00612; IQ; 2.
PF00063; myosin\_head; 1.
PF02736; Myosin\_N; 1.
PF01576; Myosin\_tail; 1.

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MYHD_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                               The human extraocular muscle myosin heavy chain gene (MYH13) maps to the cluster of fast and developmental myosin genes on chromosome 17."; RL Genomics 54:188-189(1998).

CC -!- FUNCTION: MUSCLE CONTRACTION.

CC -!- FUNCTION: MUSCLE CONTRACTION.

CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC -!- SUBUNIT: MUSCLE HYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR ENCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR ENCATION: Thick filaments of the myofibrils.

CC -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CC -!- DOMAIN: THE RODLIKE TAIL SEQUENCE OF A HEPTAPEPTIDES,

CC -!- CYCLES OF A 28-RESIDUE REPEAT PRATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CC -!- MISCALLANGOUS: EACH MYOSIN THE SI DOMAIN ARE SELECTIVELY

CC -!- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY

CC -!- MISCELLANGOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

CC MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE

SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9UKX3; 095252;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                   EMBL; AF111782; AAD29948.1; EMBL; AF075248; AAC83241.1; HSSP; P08799; LMND.
                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99318869; PubMed=10388558; Weiss A., Schiaffino S., Leinwand L.A. "Comparative sequence analysis of the
                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99026150; PubMed=9806854;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                             or send an
                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Winters L.M., Briggs M.M.,
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                                                                                                                   InterPro;
                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                         ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                       SUBFRAGMENT (S2)
                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NARQQLERQNKDLKAKLQELEGAVKSKFKATISALEAKIGQLEEQL
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                                                                                                                                                   603487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain family: implications for functional diversity.";
l. Biol. 290:61-75(1999).
                                                                                                                                                                                                                                           requires a license agreement (See an email to license@isb-sib.ch).
                                                                                IPR004009;
IPR002928;
IPR001609;
                                                                                                                                      IPR000048;
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                                                                               Myosin_N.
Myosin_tail.
myosin_head.
                                                                                                                                      IQ.
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Best Local S
Matches 84
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P12844;
01-OCT-1989 (
01-OCT-1989 (
16-OCT-2001 (
Myosin heavy
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NP_BIND
DOMAIN
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MOD_RES
                                                 SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=89178677; PubMed=2926820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multigene
DOMAIN
     heavy chain gene family.";
J. Mol. Biol. 205:603-613(1989).
                          Dibb N.J., Maruyama I.N., Krause M., "Sequence analysis of the complete C.
                                                                                            Rhabditidae; Peloderinae; NCBI_TaxID=6239;
                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                             Caenorhabditis elegans
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SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1296
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                                                                                                                                                                                                                                                                                                                            TSGSQHCLPKKLCLERARSPMQNVLKKVHKVSKPESQLSLGGQRCVGELDEELAGAFPLF
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9 (Rel. 12, Last
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vy chain A (MHC
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Last annotation update)
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1Q.
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                                                                   ----AESRSSTDVVRI
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7; Mismatches
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Pred. No. 0.
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                           Caenorhabditis
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                                                                                                                  Rhabditida;
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Pfam; PF00063; myosin_head; 1.
Pfam; PF002736; myosin_N; 1.
Pfam; PF01576; myosin_tail; 1.
Pfam; PF00193; myosin_head; 1.
PRINTS; PR00193; myosin_head; 1
SMART; SM00015; IQ; 1.
SMART; SM000242; MYSC; 1.
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-i- SUBUNIT: MUSCLE EXYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-i- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

-i- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILE.

-i- PIM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

-i- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBBRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X08067; CAA30856.1; -. PIR; S02771; S02771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR002928; Myosin_tail.
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                                             929
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21.28;
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ATP.
ACTIN-BINDING.
ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                    WW.
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O1-JUN-1994 (Rel. 29, o
O1-FEB-1996 (Rel. 33, i
16-OCT-2001 (Rel. 40, i
Myosin heavy chain, noi
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Simons M., Wang M., McBride O.W., Kaw
Gdula D., Adelstein R.S., Weir L.;
"Human nonmuscle myosin heavy chains
on different chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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"Cloning of the cDNA encoding human nonmuscle myosin heavy
analysis of human tissues with isoform-specific antibodies.
J. Muscle Res. Cell Motil. 16:379-389(1995).
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=96025307; PubMed=7499478;
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CHAPNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2),

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A.28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL CIERD OF A TO TO THE CONTROL OF TOWATH
                            SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR SIMILARITY: CONTAINS 1 IQ DOMAIN.
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0, nonmuscle type B (Cellular myosin
0, myosin heavy chain-B) (NMMHC-B).
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SMART; SM00015; TQ; 1.
SMART; SM00242; MYSc; 1.
PROSITE; PS50096; TQ; 1
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Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF01578; MYOSINHEAVY;
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InterPro; IPR002017;
InterPro; IPR001609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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SDNARQQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQL
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                                         KLCLERARSPMQNVLKKVHKVSKPESQLSLGG-QRCVGELDEEL
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21.8%;
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COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
8 MW; B2BB87FF35EA124F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 179.5; DE Pred. No. 0.082;
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J. Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no rest used by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacciaromycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=X210V-10,
MEDLINE=91185402; PubMed=2010462;
    965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-8 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-1993) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hostetter M.K., Herman
Kendrick K.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 782-1790 FROM N.A.
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Yamasaki M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=X2180-1A;
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                                      56 KTIINKLEEDLAQEEENVLDA-EFLKNE----LDSVKAQLSQKDREKRDSQAIIDTLRDT
                                                                                                               Local
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                                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3L; X54378; CAA38253.1; 3L; L03188; AAB00143.1; 3L; U53668; AAB66659.1; A38455; A38455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPICOLLED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CESSIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL ER AND THE GOLGI COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; P80220; 1DIP.
S0002216; USO1.
PPro; IPR002017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: REQUIRED
KSLANN-YKDMQAENESLIKAVEESKNESSIQLSNLQNKIDSMSQEKENFQIERGSIEKN 1023
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18.1%;
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cerevisiae.";
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Query Match Best Local S Matches 74

Similarity

**7** 20

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Score 177.5; Pred. No. 0.

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Conservative

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Hypothetical SEQUENCE 1
                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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          RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.,
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RA Bagguley C., Bailey J., Barlow K., Bates K.N., Beasley O., Bird C.P.,
RA Blakey S., Bridgeman A.M., Buck D., Burgess J., Burrill W.D.,
RA Blukey S., Bridgeman A.M., Buck D., Burgess J., Burrill W.D.,
RA Blukey S., Bridgeman A.M., Buck D., Burgess J., Burrill W.D.,
RA Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., Corby N.,
RA Collier G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
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RA Colley V., Cole C.G., Collier G.F., Coward M.E.,
RA Hatthews L., McCann O.T., McClay J., Mclaren S., McCre A.V.,
RA Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V.,
RA Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V.,
RA Ramsey Y., Rogers J., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
RA Milnes S., Kounn R.M., Vaudin M., Wall M., Wallis J.M.,
RA Miller T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R.,
RA Mitsuyama S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S.,
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RA Sulan D., Song L., Wang C., Wang Y., Wang Z., White J., Malaj E.,
RA Muth., Yao Z., Zhan M., Zhang S., Chissoe S., Murray J., Malaj E.,
RA Mitsuyama D., Cordes M., Du Z., Fulton L., Goela D.,
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15-DEC-1998 (Rel. 37, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain, Myosin heavy chain-A) (NMMHC-A).
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Mammalia; Eutheria;
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MEDLINE-90138958; PubMed=1967836;
Saez C.G., Myers J.C., Shows T.B., Leinwand L.A.;
"Human nonmuscle myosin heavy chain mRNA: generat through alternative polyadenylylation.";
through alternative polyadenylylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Human nonmuscle myosin heavy chains on different chromosomes."; Circ. Res. 69:530-539(1991).
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         -!- SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MIG), 2 ALKALI LIGHT CHAIN SUBUNITS (MIG) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MIG-2),
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALHHA-HELICAL COLLED COLLS.
-!- DISEASE: DEFECTS IN MYH9 ARE THE CAUSE OF MAY-HEGGLIN ANOMALY (MHA), AN AUTOSOMAL DOMINANT MACROTHROMBOCYTOPENIA CHARACTERIZED BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS.
-!- DISEASE: DEFECTS IN MYH9 ARE THE CAUSE OF FECHTNER SYNDROME (FINS), AN AUTOSOMAL DOMINANT MACROTHROMBOCYTOPENIA, CHARACTERIZED BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS.
-!- DISEASE: DEFECTS IN MYH9 ARE THE CAUSE OF FECHTNER SYNDROME (FINS), AN AUTOSOMAL DOMINANT MACROTHROMBOCYTOPENIA CHARACTERIZED BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS.
--- BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE SENSORIHEURAL DEAFNESS, CATARACTS AND NEPHATTIS.
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Ghiggeri G.M., Ravazzolo R., Savino M., Del V
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Nat. Genet. 26:106-108(2000).
-!- FUNCTION: CELLULAR MYOSIN
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"Mutation of MYH9, encoding non-muscle
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MEDLINE=20428193; PubMed=10973260;
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PubMed=10973259;
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InterPro; IPR002017; Spectrin.
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pfam; pF00612; IQ; 1.
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MEDLINE-20570466; PubMed-11121031;

KAWASSHIMA T., AMAROO N., KOİKE H., MAKİNO S.-I., HİGUCHİ S.,

KAWASSHIMA T., AMAROO N., KOİKE H., MAKİNO K., Kanehori K., Kawamot

KawaShiMa-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamot

KunoshiDa T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

*NICANABA T., AMAROO N., Maramaki H., Makino K., Suzuki M.;

*Archaeal adaptation to higher temperatures revealed by genomic

sequence of Thermoplasma volcanium.*;

sequence of Thermoplasma volcanium.*;

Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

Proc. Natl. Nacd. Sci. U.S.A. 97:14257-14262(2000).
                                                                                                                                                                                                                                                                                                  RA50_THEVO
P58302;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1491
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                                                                                                                                                                                             Thermoplasma
                                                                                                                                                                                                         Archaea; Euryarchaeota;
                                                                                                                                                                                                                       Thermoplasma volcanium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1251
                                                                                                                                                                             NCBI_TaxID=50339;
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rad50/mrell complex possesses
                                                                                                                                                                                                                                                                                                                                                                                                                                    KAKSKOKVRIKTVSSASOPKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLKK------QMKFLEQ
                                                                                                                                                                                                                                                                                                                                                                                                          ELEDERKORSMAVAARKKLEMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKLCLERA----RSPMQNVL-----KKVHKVSKPESQLSLGGQRC---VGELDEELAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QCRIQVGKKTIINKLFFDLAQEEENV------LDAEF--LKNELDSVKAQLSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFPLFIRNAVLGOKOPNRTTAESRSSTDVVRIGFDGLGGRTKFIQPRDTTIIRPV-PVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKAELERLNKQFRTEMEDLMSSKDDVGKSVHELEKSKRALEQQVEEMKTQLEELEDELQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HQRQSACNLEKKQKKFDQLLAEEKTISAKYAEERDRAEAEAREKETKALSLARALEEAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKMEDSVGCLETAEEVKRKLQKDLEGLSQRHEEKVAAYDKLEKTKTRLQQELDDLLVDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDTQELLQEENRQKLSLSTKLKQVEDEKNSFREQLEEEEEAKHNLEKQIATLHAQVADMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEMIRDMGV----GQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKQKRDLGEELEALKTELEDTLDSTAAQQELRSKREQEVNILKKTLEEEAKTHEAQIQEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELKMQLAKKE--EELQAALARVEEEAAQKNMALKKIRELESQISELQEDLESERASRNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKSDDPPGNLEPASATN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAQLQELQVKFNEGERVRTELADKVTKLQVELDNVTGLLSQSDSKSSKLTKDFSALESQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQKHSQAVEELAEQLEQTKRVKANLEKAKQTLENERGELANEVKVLLQGKGDSEHKRKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQ-----QIELLLQS-----QRSEV
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                                                                                                                                                                                                                                                     repair rad50
                                                                                                                                                                                                         Thermoplasmales; Thermoplasmaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                          1618
                                                                                                                                                                                                                                                                                                                                                                                                                                      465
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETVSRLVFESPA---PVEMMNPRLHQPPFGDEIDLN
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single-strand endonuclease activity
                                                                                                                                                                                                                                                        ATPase
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                                                                                      Kawamoto
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Best Local
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MYSN_ACACA

STANDARD;
P05659;
01-NOV-1988 (Rel. 09, Cr
01-NOV-1988 (Rel. 09, La
16-OCT-2001 (Rel. 40, La
16-OCT-2011 heavy chain, n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete NP_BIND 30 ATP (BY SIMILARITY).

DOMAIN 171 737 COILED COIL (POTENTIAL).

SEQUENCE 895 AA; 103223 MW; 4A47DA9287E82D3A CRC64;
Eukaryota; Acanthamoebidae;
NCBI_TaxID=5755;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003439; ABC_
InterPro; IPR000875; Cecr
InterPro; IPR001238; RecF
                                              Acanthamoeba castellanii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP000991; BAB59370.1; -.
                                                                                                                                                                                                                                                                                 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
SUBUNIT: Forms a con
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and ATP-dependent double-strand-specific exonuclease activity Rad50 provides an ATP-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                 LSLGGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNINKDVFLTSIFVRQGEMDALVSKDPAERKKILDEILNIDRLEAGYLLLKEVIDDLTAN
                                                                                                                                                                                                                      AMLSGR
                                                                                                                                                                                                                                                                                                            HQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPKKLCLERARSPMQNVLKKVHKVSKPESQ
                                                                                                                                                                                                                                                                                                                                         RSSLKEDEDNYQSAVRNIENIKKWIENEEKEIERMSAFISEILKIQEITP--
                                                                                                                                                                                                                                                                                                                                                            KLELRSAQKDLQSADQEITSLRKKSDDPPGNLEPASATNETVSRLVFESPAPVEMMNPRL
: |: : | | : : | | :: | |
                                                                                                                                                                                                                                                                                                                                                                                                    NEITEYINLKKDLGSLSEITEGLKSDLSKYDEAHRKLEDLQSFRSEFLEKKKRKEDLDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQAREEAHRLKCKMKTMEQIELLL---QSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSDYDYLKNELQSKI----NEIDNNNKQIEELESKLRLIEPEIKALEEEINIKENKKD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSQKDREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLKKQMKFLEQRQDET 149
                                                                                                                                                                                                                                                                                ------RAEINSSLMQIEG-----KIASLNASIDAMRS-----HKMEVEENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -HLNEELHRLNAQLETIKKYEMELAESQSRKASIEMEVVKLPSIEEELKRLENNAAVVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00470; RecF; 1
PF02463; SMC_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 20.5
75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    EYENLKEARKATGELADRLK------
                                                                                                                                                                                                                                                   372
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TY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMC_N.
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                                                                           Last sequence update)
Last annotation updat
                                                                                                           Created)
                                                              non muscle.
                                                (Amoeba)
                                 Acanthamoeba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 176.5; DE Pred. No. 0.049;
                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                            update)
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Query Match
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Matches 81
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SEQUENCE
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Pfam; PF02736; Myosin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                SMART; SM00015; IQ; 1
SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                              PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                           Pfam; PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                  DOMAIN
                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                               Myosin;
                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                      ProDom;
                                                                                                                                                                                                                                                                                                                              InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
                                                                                                                                                                                                                                                                                                                                                  PIR; A27224; A27224.
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y00624; CAA68663.1;
                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=87308395;
                                                                                                                                        DOMAIN
                                                                                                                                                                                                                    Methylation;
                                                                                                                                                                                                                                                                                                                    InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS REGION IS INTERRUPTED BY A HINGE AND JOINED BY A NONHELICAL TAILPIECE WHERE THE REGULATORY PHOSPHORYLATION SITES RESIDE.
MISCELLANDOUS: THE HINGE REGION MAY PLAY A KEY ROLE IN MEDIATING THE EFFECT OF HEAVY CHAIN PHOSPHORYLATION ON ENZYMATIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                             European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 2 IQ DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
   81;
            Similarity
                                                                                                                                                                                                                                Coiled
                                                                                                                                                                                                                                                                    PD000355; myosin_head;
                                                                                                                                                                                                                                        PS50096;
                                                  790
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                                                                                                                                                                                                                                                                                                                                                                                                 license agreement (See
                                                                                                                                                                                                                    Actin-binding; ATP-binding; Calmodulin-binding; ion; Phosphorylation; Multigene family.
            7
24
                                                  171201
           1.58;
  63;
                                                  WW;
Score 176.5;
Pred. No. 0.08
3; Mismatches
                                                                             ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (TRI-) (POTENTIAL)
ALKYLATION (SH-1) (POTENTIAL).
PHOSPHORYLATION.
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COILED COIL
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W; 2CE49BE51173D17E
                                                                     PHOSPHORYLATION
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           No. 0.
                                                                                                                                                           MEROMYOSIN (LMM)
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MBL outstation -
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01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Myosin heavy chain, skeletal muscle (Fragments).
Oryctolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                            Lu R.C., Wong A.;
"The amino acid sequence and stability predictions region in myosin subfragment 2.";
J. Biol. Chem. 260:3456-3461(1985).
 the
                                                                                                                                                                                                                   Maeda K., Sczakiel G., Wittinghofer A.; "Characterization of cDNA coding for the complete light meromyosin portion of a rabbit fast skeletal muscle myosin heavy chain."; Eur. J. Biochem. 167:97-102(1987).
                                                                                                                                                                                                                                                                                                                                                                                    myosin.";
Biophys. J. 33:148A-148A(1981).
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Capony J.-P., Elzinga M.;
"The amino acid sequence of A 34,000 dalton
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MEDLINE-85131142; Pu
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                                                                                 FUNCTION: MUSCLE CONTRACTION.

SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMALN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                     SUBFRAGMENT (S2).
SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC WHICH DICTATE THE ALPHA-HELICAL COILED-COIL:
 European
         SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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01-JUL-1989
15-JUL-1998
                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
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Myosin; Muscle protein; Coiled
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                                382 LAGAFPLFIRNAV-LGOKOPNRTTAESRSSTDVVRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              paramyosin.";
J. Mol. Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

DOMAIN: FOR MOST OF ITS LENGTH, PARAMYOSIN APPEARS TO FORM AN ALPHA-HELICAL COILED COIL AND SHOWS THE HEPTAD REPEAT OF HYDROPHOBIC AMINO ACID RESIDUES AND THE 28-RESIDUE REPEAT OF CHARGED AMINO ACIDS CHARACTERISTIC OF MYOSIN HEAVY CHAINS. HOWEVER, PARAMYOSIN DIFFERS FROM MYOSIN IN HAVING NON-HELICAL EXTENSIONS AT BOTH TERMINI AND AN ADDITIONAL "SKIP" RESIDUE THAT INTERRUPTS THE 28-RESIDUE REPEAT. THE DISTRIBUTION OF CHARGED RESIDUES IS ALSO DIFFERENT FROM MYOSIN HEAVY CHAINS.

PTM: PHOSPHORYLATED ON SERINE RESIDUES IN THE NON-ALPHA-HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401. B101. 207:451-454(1989).
FUNCTION: PARAMYOSIN IS A MAJOR STRUCTURAL COMPONENT MANY THICK FILAMENTS ISOLATED FROM INVERTEBRATE MUSCI SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation burney and Bioinformatics institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: HIGH, TO MYOSIN HEAVY CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-TERMINAL REGION
                                                                                                                                                                                                                                                                                                                                                                                                          S04027; S04027.
ETAELEMTVDNLNRANTEAQ---KTIKKQSEQLKILQASLEDTQRQLQQVLDQYALAQRKV
                            QMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELL---LQSQRSEVEEMIRDMGVGQSAV
                                                            ELQALRIEMERRI
                                                                                                                    KLHDELHEAKEALADANRKLHELDLENARLAGEIRELQTALKEADAQRRDAENRAQRALA
                                                                                                                                                                                                                                                                                                                                                                                              P80220;
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                                                                                        QAIIDTLRDTLEERNATVESLQNALN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                        an email to license@isb-sib.ch).
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                                                                                                                                                                                                Similarity
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ol. 211:665-665(1990).
                                                                                                                                                                                                                                                         882
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872
143
632
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                      Muscle protein; Thick filament; Myosin; Phosphorylation
1 47 NONHELICAL REGION (POTENTIAL).
48 871 COILED COIL (POTENTIAL).
872 882 NONHELICAL REGION (POTENTIAL).
143 143 INTERCHAIN (POTENTIAL).
632 632 INTERCHAIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207:311-333(1989).
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                                                          LQEKEEEMEALRKNLQFEIDRLIAALADAEARMKSEI--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       license agreement (See http://www.isb-sib.
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21.8%;
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Pred. No. 0.05
65; Mismatches
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                                                                                                                                                                                                                                                         rerchain (POTENTIAL).
894C4BFF4A670C5F CRC64;
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Pfam; PF00612; IQ; 1.
Pfam; PF00613; myosin_head; 1.
Pfam; PF02736; myosin_k; 1.
Pfam; PF01576; myosin_tail; 1.
Pfam; PF00193; myosin_head; 1.
PRINTS; PR00193; myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type A)
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Q62812;
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COO1 O.H., Park C., Itoh K., Adelstein R.S., Beaven M.A.; Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-i-FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS.
CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myosin heavy chain, nonmuscle type A (Cellular myosin type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAT
                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                               modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                       InterPro; IPR000048; IQ.
InterPro; IPR004009; Myc
InterPro; IPR002928; Myc
InterPro; IPR001609; myc
                                                                                                                                                                                      EMBL; U31463; AAA74950.1; -. HSSP; P10587; 1BR1.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC 2).
REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPT CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 10 DOMAIN.
                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                             myosin_head;
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Amphibia; Batrachia; Anura; Xenopodinae; Xenopus. NCBI_TaxID=8355;
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                                                                                     Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniat
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112; Mismatches
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ALKYLATION (SH-2) (POTENTIAL).
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RESULT 23
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MYH8\_HUMAN STANDARD; P13535; Q14910; O1-JAN-1990 (Rel. 13, Created)

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SEQUENCE
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InterPro; IPR003395; SMC_N.
Pfam; PP02483; SMC_C; 1.
Pfam; PP02463; SMC_N; 1.
Mitosis; ATP-binding; Coiled
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Hirano T., Mitchison T.J.;
"A heterodimeric coiled-coil protein required
condensation in vitro.";
Cell 79:449-458(1994).
-!- FUNCTION: REQUIRED FOR BOTH ASSEMBLY AND S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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  ERYNDLMKRKRIVENDKSKI----
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ALA/ASP-RICH (DA-BOX).
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MEDLINE-95324556; PubMed-7601129;
Jullian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schi Stedman H.H., Rubinstein N.A.;
"Characterization of a human perinatal myosin heavy-chain transcript.";
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Gene 89:2
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Karsch-Mizrachi I., Feghali R., Shows T.B. Jr., Leinwand L.A.;
"Generation of a full-length human perinatal myosin heavy-chai
                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arnold H.H.;
"Identification of three
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MEDLINE=95324556; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation and characterization of the human perinatal MHC Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-46 FROM N.A.
Esser K., Tidhar A., Myszkowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reghali R., Leinwand L.A.;
molecular genetic characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89234168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 860-1937 FROM N.A.
MEDLINE=89234168; PubMed=2715179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bober E.,
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TISSUE-Skeletal mu
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MYH8.
                                                                                                                                                                                                                                                                                                                            SUBUNIT: MUSCLE MYSSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBERRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                           SPLIT FURTHER INTO 2 SUBFRAGMENT (S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89:289-294(1990).
M36769;
Z38133;
                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             perinatal myosin heavy chain.";
ll Biol. 108:1791-1797(1989).
                                                                  s requires a license agreement (S
an email to license@isb-sib.ch).
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AAC17185.1;
CAA86293.1;
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Primates;

    Last sequence update)
    Last annotation update)
    skeletal muscle, perinatal

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                                                                                        (See http://www.isb-sib.ch/announce/
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pfam; PF02736; Myosin_N; 1.
pfam; PF01576; Myosin_tail; 1.
pRINTS; PR00193; MYOSINHBAVY.
PTODOm; PD000355; myosin_head;
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InterPro; IPR002928;
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                                                                                                                                                            ALDKKQRNFDKVLSEWKQK----YEETQAELEASQKESRSLSTELFKVKNVYEESLDQL
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M35250; AAA36346.1; -
AF067143; AAC21557.1;
A30220; A30220.
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SM00242; MYSC;
E; PS50096; IQ;
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77; Conserv
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Myosin_N.
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myosin_head
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A -> R (IN REF. 2),
E -> Q (IN REF. 1 AND 4).
M -> N (IN REF. 3),
N -> H (IN REF. 1 AND 4).
MC -> DGG (IN REF. 1 AND 4).
MC -> DGG (IN REF. 1 AND 4).
K -> Q (IN REF. 1 AND 4).
K -> Q (IN REF. 1 AND 4).
K -> Q (IN REF. 1 AND 4).
C -> DGH (IN REF. 1 AND 4).
C -> DGH (IN REF. 1 AND 4).
C -> DGH (IN REF. 1 AND 4).
C -> DGH (IN REF. 1 AND 4).
C -> DGH (IN REF. 1 AND 4).
C -> DGH (IN REF. 2).
C -> H (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 172.5;
Pred. No. 0.18
79; Mismatches
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METHYLATION (TRI-)
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(SH-2)
(REF. 2)
REF. 1
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   use by non-profit institute. There are no restrictions modified and this statement is not removed. Usage by and for contitles requires a license agreement is removed or send an contilled and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-9533646; PubMed-7612011;
Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., J. A., Fertig N., Medsger T.A. Jr., J. A., Novel cell-cycle-dependent 350-kba nuclear protein: domain sufficient for nuclear localization.";
Biochem. Biophys. Res. Commun. 212:220-228(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CENF_HUMAN STANDARD; PRT; 3210 AA. P49454; Q13246; Q13171; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
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"Characterization of the kinetochore binding domain interactions with the kinetochore proteins CENP-F ar
                                                                                                                                                                                                                                                                                                                                                                                          Zhu X., Chang K.-H., He D., Mancini M.A., Brinkley W.R., "The C terminus of mitosin is essential for its nuclear centromere/kinetochore targeting, and dimerization."; J. Biol. Chem. 270:19545-19550(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95379848; PubMed=7651420;
Zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., C
Jones D., Yang-Feng T.L., Lee W.-H.;
"Characterization of a novel 350-kilodalton nuc
that is specifically involved in micotic-phase
that is specifically involved in micotic-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Breast carcinoma;
MEDLINE-95348175; PubMed-7542657;
Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.;
"CENP-F is a protein of the nuclear matrix that assemble:
kinetochores at late G2 and is rapidly degraded after mi
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Zhu X., Chang K.-H.,
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                                                                                                                                                                         Cell Biol. 143:49-63(1998).

FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION, INVOLVED CHROMOSOME SECREGATION DURING MITOSIS. INTERACTS WITH RETINOBLASTOMA PROTEIN (RB), CENP-E AND BUBRI.

SUBUNIT: HOMO- OR HETERODIMER.

SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE NUCLEOLUS).

REDRGANIZATION TO THE KINETOCHORE/CENTROMERE (CORONAL SURFACE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell Biol. 130:507-518(1995).
                                                        s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest
                                                                                                                                            THE OUTER PLATE) AND THE SPINDLE DURING MITOSIS. DEVELOPMENTAL STAGE: GRADUALLY ACCUMULATES DURING
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license@isb-sib.ch)
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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EMBL; U30872; AAA82935.1;
EMBL; U25725; AAA86889.1;
HSSP; P02649; 1LE4.
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1130 AA;
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121 79 COILED COIL (POTENTIAL).
805 1061 COILED COIL (POTENTIAL).
130 AA; 131485 MW; B0FDZEFE3D99FB09 CRC64;
                                chain,
                                                                                                   STANDARD;
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    Last sequence update)
    Last annotation update)
    skeletal muscle, fetal (Myosin heavy chain IIb)

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Pred. No. 0.12
38; Mismatches
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RY "Comparative sequence analysis of the complete human sarcomeric myosin RT heavy chain family: implications for functional diversity.";

RI J. Mol. Biol. 290:61-75(1999).

C: HENCTION: MUSCLE CONTRACTION.

C: SUBBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC).

C: HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC).

C: HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC).

C: SUBCELLULAR IOCATION: Thick filaments of the myofibrils.

C: POMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

C: CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

C: CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

C: CYCLES OF A 28 RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE RESULTED FOR MYOSIN ATPASE ACTIVITY.

C: PTM: TWO CYSTEINE RESULTED FOR MYOSIN ATPASE ACTIVITY.

C: MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT CHAIN SUBPRAGMENTS (S1) AND 1 ROD-SHAPED

C: SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                Query Match
Best Local S
Matches 78
                                                                                                                                                                                                                                                                                                                       Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_u; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                     ProDom; PUVVVI
SMART; SM00015; IQ; I.
SMART; SM00242; MYSC; I.
SMART; SM00242; MYSC; I.
                                                                                                                                             DOMAIN
NP_BIND
SEQUENCE
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InterPro; IPR002928;
InterPro; IPR001609;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch)
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1270 QQRLINEL---SAQKARLHTESGEFSRQLDEKDAMVSQLSRGKQAFTQQIEELKRQLEEE 1326
                                                                                                                                                                                                                                            Calmodulin-binding; ATP-binding; Methylation;
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SIMILARITY: CONTAINS 1
SIMILARITY: CONTAINS 1
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                                KKTIINKLFFDLAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEER 114
                                                                Similarity
78; Conser
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186
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Myosin_tail.
myosin_head.
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MW;
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Pred. No. 0.22
33; Mismatches
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IQ.
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
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115

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T Riol. Chem. 265:2603-2612(1990).
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DESP_HUMAN STANDARD; PRT; 2871 AA.

P15924; Q14189; Q75993; Q9UHN4;

01-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen).
                                                                                                                                                                                        Green K.J., Parry D.A.D., Steinert P.M., Virata Angst B.D., Nilles L.A.; J. Biol. Chem. 265:11406-11407(1990).
 "Striate palmoplantar keratoderma resulting haploinsufficiency.";
J. Invest. Dermatol. 113:940-946(1999).
[6]
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                                                                            Whittock N.V., Ashton G.H., Keane F.M., Eady R.A.J., Mc
                                                                                                                 MEDLINE=20062965;
                                                                                                                                                       SEQUENCE OF 2854-2871 FROM N.A.
                                                                                                                                                                                                                                                 MEDLINE=90361712; PubMed=2391353;
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MEDLINE-90153880;
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                                                                                                                   PubMed=10594734;
                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=1689290;
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                                                                            H., Dopping-Hepenstal P.J.,
McGrath J.A.;
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   Kowalczyk A.P., Bornslaeger E.A., Borgwardt J.E., Palka H.L., bhaliwal A.S., Corcoran C.M., Denning M.F., Green K.J.;
"The amino-terminal domain of desmoplakin binds to plakoglobin clusters desmosomal cadherin-plakoglobin complexes.";
J. Cell Biol. 139:773-784(1997).

-i- FUNCTION: MAJOR HIGH MOLECULAR WEIGHT PROTEIN OF DESMOSOMES.
INVOLVED IN THE ORGANIZATION OF THE DESMOSOMAL CADHERIN-PLAKOGLOBIN COMPLEXES INTO DISCRETE PLASMA MEMBRANE DOMAINS
THE ANCHORING OF INTERMEDIATE FILAMENTS TO THE DESMOSOMES.
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InterPro; IPR002017; Spectrin.
Pfam; PF00681; Plectin_repeat; 20.
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HSSP; P01100; 1FOS.
MIM; 125647; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentities requires a license.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                   Structural
                                                                                                                                                                                                                                                                                                                                                                                                 Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J05211; AAA35766.1; -...
EMBL; AF139065; AAF19785.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KERATODERMA II (PPKS2, KPPS2 OR SPPK2), CHARACTERIZED BY SKIN THICKENING IN THE PALMS (LINEAR PATTERN) AND THE SOLES (ISLAND-LIKE PATTERN) AND FLEXOR ASPECT OF THE FINGERS; AND RARELY BY ABNORMALITIES OF THE NAILS, THE TEETH AND THE HAIR.
SIMILARITY: CONTAINS 17 PLECTIN REPEATS.
SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRATIFIED ORIGIN.

STRATIFIED ORIGIN.

DOMAIN: THE N-TERMINAL REGION IS REQUIRED FOR LOCALIZATION TO THE DESMOSOMAL PLAQUE AND INTERACTS WITH THE N-TERMINAL REGION OF DLAKOPHILIN 1. THE C-TERMINAL REGION INTERACTS WITH INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: INNERMOST PORTION OF THE DESMOSOMAL PLAQUE ALTERNATIVE PRODUCTS: 2 ISOFORMS; DPI/DP1 (SHOWN HERE) AND DPII/DP2; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: DPI IS APPARENTLY AN OBLIGATE CONSTITUENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: DEFECTS IN DSP ARE A CAUSE OF STRIATE PALMOPLANTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALL DESMOSOMES; DPII RESIDE PREDOMINANTLY IN TISSUES
                                                                                                                                                                                                                                                                                                                                                                                                                      SM00250; PLEC;
SM00150; SPEC;
                                                                                                                                                                                                                                                                                                                                                                                                  Coiled coil;
                                                                                                                                                                                                                               1057
1946
347
858
1018
2009
2046
                                                                                                                                                                                                                                                                                                                                                                                   protein;
 11056
11945
2871
952
1945
2083
2083
2159
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22137
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23664
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2402
2647
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                                                                                                                                                                                                                                                                                                                                                                                   Alternative splicing.
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113.
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                                                                                                                                                                                                                                                                     (POTENTIAL)
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Best Loc
Matches
                                                    Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
NCBI_TaxID=9606;
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VARSPLIC
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                    _HUMAN
TMF1_HUMAN
P82094;
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30-MAY-2000
16-OCT-2001
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REPEAT
  MEDLINE=93028466; PubMed-Garcia J.A., Ou S.-H.I.,
                                                                                                          TATA element
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                      SEQUENCE FROM N.A., AND FUTISSUE-Cervical carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQWFETAPSRTCPQCRIQVGKKTIINKLFFDLAQEEENVLDAEF---
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                                                                                                                                                                                                                                          OPRDITIIRPVPVKSKAKSKQKVRIKTVSSASQPKL
                                                                                                                                                                                                                                                                 TERSRYQREIDK-----
                                                                                                                                                                                                                                                                                    LGGQRCVGELDEELAGAFPLFIRNAVLGQKQPNRTTAESRSSTDVVRIGFDGLGGRTKFI 428
                                                                                                                                                                                                                                                                                                                                TSGSQHCLPKKLCLERARSP------MQNVLKKVHK------VSKPESQLS
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3; Conservative
                                                     s (Human).
Metazoa; Chordata; C
---heria; Primates; (
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1195
905
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2871
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(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
modulatory factor (TMF).
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2724
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1794
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A; 331771
            PubMed=1409643;
                                  AND FUNCTION
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18.0%;
 Wu F.,
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MISSING (IN ISOFORM D
R > A (IN REF. 2).
D -> R (IN REF. 3).
SV -> RL (IN REF. 2).
MW; 5639B5B7CD4690B7
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PLECTIN 16.
PLECTIN 17.
6 X 4 AA TANDEM I
INTERACTS WITH PI
PLAKOGLOBIN.
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Pred. No. 0.34;
0; Mismatches
                                                                Craniata; Vertebrata;
Catarrhini; Hominidae;
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  Lusis
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 А.J.,
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                                                                 Hominidae;
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DPII).
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 R.S.,
                                                                            Euteleostomi;
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AND JUNCTION
  Gaynor
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RESULT 29
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Best Local S
Matches 107
                                       DOMAIN
DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and chromosomal mapping of a human immunodeficiency 'TATA' element modulatory factor.";
Proc. Natl. Acad. Sci. U.S.A. 89:9372-9376(1992).
PROUCTION: THIS PROTEIN BINDS THE HIV-1 TATA ELEMENT AND ITEANSCRIPTIONAL ACTIVATION BY THE TATA-BINDING PROTEIN (T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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sapiens
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                                                                                                                                                                                                                                                                                    LSDRLGESQTLLAAAVERERAATEELLANKIQMSSMESQNSLLRQENSRFQAQLESE---
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07; Conservative
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                          interacting
                                                                                                                                                                                                                            -KNRLCKLEDENNRYQVELENLKDEYVRTLEETRKEKTLLNSQLE--MERMKVEQ
                                       (Rel. 40, Created)
(Rel. 40, Last seq
(Rel. 40, Last ann
(Human)
                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.1%;
                                         Last sequence update)
Last annotation updat
                         Last annotation update) protein 1 (HIP-I) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wanker E.E., Rovira C., Scherzinger E., Tait D., Colicelli J., Lehrach H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97227296;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                 European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: CYTOPLASMIC. MEMBRANE-ASSOCIATED PROTEIN. ALTERNATIVE PRODUCTS: 2 ISOFORMS; HIP1-1 AND HIP1-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE SLA2 FAMILY
                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: THE AFFINITY OF THE HUNTINGTIN PROTEIN-HIP1
INTERACTION IS INVERSELY CORRELATED TO THE LENGHT OF THE
POLYGLUTAMINE TRACT ADDED TO THE HUNTINGTIN PROTEIN IN HUNTINGTON
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                                                                                                                                                           s requires a license agreement ( an email to license@isb-sib.ch)
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Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
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-i- SIMILARITY: TO YEAST YHLO10C AND S.POMBE SPAC16E8.13
-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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SMART; SM00290; ZnF_UBP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
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InterPro; IPR001841; Znf_ring.
InterPro; IPR001607; zf-UBP.
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or send an email to license@isb-sib.ch).
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LRHDMEQTMSKMEKTAYAQVENLEHQLTER-----STELKSLKGDLDDTVTARKVAE- 1125
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PS50089; ZF_RING_2; 1.
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MYSS_CYPCA
                                                                                               This
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"Structural differences in the crossbridge head of temperature-"structural differences in the crossbridge head of temperature-
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Q90339;
                                                                                                                                                                                                                                                                                                                                                                                      different primary structures in carp fast skeletal muscle.", Biochem. Biophys. Res. Commun. 208:118-125(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Cyprinus.
                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
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Uozumi T., Hirono I., Aoki T.;
"Temperature acclimation induces light meromyosin isoforms with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acclimation.";
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MEDLINE=97352533; P
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Myosin heavy chain, fast skeletal muscle.
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Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
"CDNA cloning of myosin heavy chain isoforms from carp fast skeletal
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                                                                                                                                                                              SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MIC), 2 ALKALI LIGHT CHAIN SUBUNITS (MIC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MIC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMANI: THE ROLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY
ALKYLATED AND ARE REQUIRED FOR MYOSIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                        SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
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Pfam; PF00612; IQ; 1.

Pfam; PF00736; MyOSin_N; 1.

Pfam; PF01736; MYOSIN_LTAil; 1.

Pfam; PF01576; MYOSINHEAVY.

PRINTS; PR00193; MYOSINHEAVY.

PRODOM; PD000355; MYOSIN-head; 1.

SMART; SM00015; IQ; 1.

SMART; SM00242; MYSC; 1.

PROSITE; PS50096; IQ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
                                         1543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myosin; Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                    399
                                                                                                         301
                                                                                                                                                                                                                                                                             135
                                                                                                                                                                                           224
                                                                                                                                                                                                                                    173
                                                                                                                                                                                                                                                                                                                     86
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                                                                                                                                                                                                                                                                                                                                                            LQCLIQWFETAPSRTCPQCRIQVGKKTIINKLFFDLAQEEENVLD-----AEFLKNELDS
Q-STLDSEVRSRNDALRV
                    QPNRTTAESRSSTDVVRI 416
                                        TALEEAEGTLEHEESKILRVQLELNQVKSEIDRKLAEKDEEM----EQIKRNSQRVIDSM 1598
                                                                                                                           VERANSLAANLDKKQRNFDKVLAEWKQKYEESQAELEGAQKEARSLSTELFKMKNSYEEA
                                                                                                                                                                                                                                                                                                                    LCLERARSPMONVLKKVHKVSKPESQLSLGGQRCVGELDEELAGAFPLFIRNA--VLGQK
                                                                                                                                                                                                                                                                                               V-AELGEQIDNLQRVKQKLEKEKSEYKMEIDDL-----TSNMEAVAKAKANLEKMCRT
                                                                                                                                                                                                                                                                                                                                         LEEISERLEEAGGATAAQIEMNKKREAEFQKMRRDL---EESTLQHEATAAALRKEQADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D89992;
D50476;
D43700;
P08799;
                                                                                  LDHLETLKRENKNLQQ-----EIS-----DLTEQLGETGKSIHELEKAKKTVESEKSEIQ
                                                                                                                                                                     RTKYETDAIQRTEELEEAKKKLAQRLQDAEESIEAVNSKCASLEKTKQRLQGEVEDLMID
                                                                                                                                                                                                             I EELKRHI EEEVKAKNALAHAVQSARHDCDLLREQY EEEQEAKAELQRGMSKANSEVAQW
                                                                                                                                                                                                                                                      LEDQLSEIKTKSDENVRQLNDMNAQRARLQTENGEFSRQLEEKEALVSQLTRGKQAYTQQ
                                                                                                                                                                                                                                                                           LKKOMKFLEORODETKOAREEAHRLKCKMKT-----MEQIELL-------
                                                                                                                                                                                                                                   LQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEAR-----
                                                                                                                                                                                                                                                                                                                                                                                  97; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                      782
812
840
178
659
761
129
699
709
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                                                                                                    -MMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPK------K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAA22069.1;
BAA09069.1;
BAA07802.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                      ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          781
811
839
1935
185
681
775
129
699
                                                                                                                                                                                  OSADQEITSLRKKSDDPPGNLEPASATNETVSRLVFESPAPVE--
                                                                                                                                                                                                                                                                                                                                                                                          7.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                      221599
                                                                                                                                                                                                                                                                                                                                                                                90;
                                                                                                                                                                                                                                                                                                                                                                                Score 169; DB
Pred. No. 0.26
90; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HINGE.
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                   METHYLATION (TRI-) (PC ALKYLATION (SH-1). ALKYLATION (SH-2). MW; 9A1244B67D63C83B C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYOSIN
IQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coil; Thick filament; Actin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                           DB
. 26;
                                                                                                                                                                                                                                                                                                                                                                                173;
                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 1935,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                 Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                  -KATGELAD-
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                       340
                                                                                                                           1492
                                                                                                                                                                                                                                                                                                1252
                                                                                  1542
                                                                                                                                                 300
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                                                                                                                                                                                                                                                                            172
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A LO COMPANDA REPRESENTATION DE LA COMPANDA DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA RESPARA REPRESENTATION DE LA COMPANDA REPRESENTATION DE LA COMPANDA
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                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR004009; Myosin_N.
InterPro: IPR002928; Myosin_tail.
InterPro: IPR001699; myosin_head.
Pfam; PP00612; IQ; 1.
Pfam; PP000612; IQ; 1.
Pfam; PP00736; myosin_head; 1.
Pfam; PP02736; Myosin_tail; 1.
Pfam; PF01576; Myosin_tail; 1.
                 MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                  Myosin;
Coiled o
                                                                                                                    DOMAIN
NP_BIND
                                                                                                                                                                                                                                                                                   SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cellular myosin.";
Proc. Natl. Acad. Sci. U.S.A. 86:7726-7730(1989).
-!- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYH9_CHICK STANDARD; PRT; 1959 AA. P14105; 01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Myosin heavy chain, nonmuscle (Cellular myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    МУН9
                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                 PROSITE; PS50096; IQ; 1.
Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P10587; 18R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M26510; AAA48974.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Intestinal epithelium;
MEDLINE=90046668; PubMed=2813355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
                                                                                              DOMAIN
                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adelstein R.S.; "Cloning of the cDNA encoding the myosin heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shohet R.V., Conti M.A., Kawamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC-2).

REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEFT CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAPPING. SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL SHAPE, AND
                                                                                                                                                                                                                  coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000048; IQ.
                      779
837
174
654
694
704
                                                                                                                                                                                                                Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.A.
                   Ą,
                                          778
808
1925
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676
694
704
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Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIALIZED FUNCTIONS SUCH AS SECRETION
                      226502
                                                                                                                                                                                                                Multigene famil
IQ.

COILED COIL (POTENTIAL).

ATP (POTENTIAL).

ACTIN-BINDING.

ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

2 MW; A75C86086FD3A1A1 CRC64;
                                                                                                                                                                                            NISOYM
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                                                                                                                                                                                            HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heavy chain) (NMMHC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration -
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Best Local
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                                                                                                                                                                                                                                                                  075665; 075666;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence up
16-0CT-2001 (Rel. 40, Last annotation
Protein CXorf5 (Protein 71-7A).
  This
                         Genomics 51:243-250(1998).

- ALTERNATIVE PRODUCTS: 2 ISOFORMS;
- PRODUCED BY ALTERNATIVE SPLICING.
- 1- TISSUE SPECIFICITY: UBIQUITOUS.
                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE-98390187; PubMed-9722947;
de Conciliis L., Marchitiello A., Wape
Giglio S., Mariani M., Consalez G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1131
                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                    HUMAN
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                                                                                           "Characterization of Cxorf5
Xp22 and encoding a protein
                                                                                                                      Giglio S., Mariani M., Ballabio A., Banfi S.;
                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                      CX05_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKQKRDLGEELEALKTELEDTLDSTAAQQELRSKREQEVTVLKKTLEDEAKTHEAQIQEM 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLKK------QMKFLEQ 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QCRIQVGKKTIINKLFFDLAQEEENV------LDAEF--LKNELDSVKAQLSQK 93
                                                                                                                                                                                                                                                                                                                                                                                                        ELEDERKQ - - - - RSIAVAARKKLE
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 SWISS-PROT entry is copyright.
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19.1%;
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                                                                                                      (71-7A),
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                                                                                          (71-7A), a containing
                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae
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Best Local
                                                                                                                                  MYH2_HUMAN STANDARD; PRT; 19
09UKX2; Q16229; Q14322;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Myosin_heavy chain, skeletal muscle, &
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the European Bioinformatics Institute. There are no restrictions
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ISOFORM 2).
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MW; C2BF4376F89E6738 CRC64;
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Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

MYH2 OR MYHSA2

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RA Ennion S., Sant'ana Pereira J., Sargeant T., Young A., Goldspink G.;

RT "Characterization of human skeletal muscle fibres according to the myosin heavy chains they express.";

RI J. Muscle Res. Cell Motil. 16:35-43(1995).

CC -!- FUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CC CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.

CC -!- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

CC -!- MISCELLANBOUS: EACH MYOSIN EARN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (ANM) LATER BE SUBTRAGMENT (S2).

CC -!- STUTLARTY CONTAINS 1 MYOSIN LIKE GLOBULAR BURDL DOMAIN
                                                        Pfam; PF00612; IQ; 2.

Pfam; PF00063; myosin_head; 1.

Pfam; PF02736; Myosin_tail; 1.

Pfam; PF01576; Myosin_tail; 1.

Pfam; PF01033; MYOSINHEAVY.

PRINTS; PR00193; MYOSINHEAVY.

PRODOM; PD000355; myosin_head; 1.

SMART; SM00015; IQ; 1.

SMART; SM00012; MYSC; 1.
         Myosin; Muscle protein; Coiled co
Calmodulin-binding; ATP-binding;
                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-99318869; PubMed-10388558;
Weiss A., Schiaffino S., Leinwand L.A.;
"Comparative sequence analysis of the complete human sarcomeric myosin heavy chain family: implications for functional diversity.";
J. Mol. Biol. 290:61-75(1999).
                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Type IIx myosin heavy chain transcripts fibers of human skeletal muscle."; Am. J. Physiol. 267:C1723-C1728(1994).
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InterPro; IPR004009;
InterPro; IPR002928;
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                                                 PS50096; IQ;
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; Myosin_tail.
; myosin_head.
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1 IQ DOMAIN.
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                                    Byrd D.A., Sweet D.J., Pante N., Konstantinov K.N., Guan T., Saphire A.C.S., Mitchell P.J., Cooper C.S., Aebi U., Gerace L.; "Tpr, a large coiled coil protein whose amino terminus is involve activation of oncogenic kinases, is localized to the cytoplasmic surface of the nuclear pore complex.";
J. Cell Biol. 127:1515-1526(1994).
                                                                                                                                                          "The human tpr gene encodes a protein of 2094 amino acids that has extensive coiled-coil regions and an acidic C-terminal domain."; Oncogene 7:2329-2333(1992).
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                                                                                                                                                 Query Match
Best Local S
Matches 74
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"MFP1, a novel plant filament-like protein with affinity
attachment region DNA."
Plant Cell 8:2105-2115(1996).
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16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CV. VFNT CHERRY; TISSUE-Fruit;
MEDLINE=97112038; PubMed=8953774;
                                                                                                                                                                                                                                               Nuclear protein; DNA-binding; Coiled coil DOMAIN 125 681 COILED COIL
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                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: NUCLEAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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           QSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSR
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                                       LEREVSKLQ------MELEETRASLQRNIDETKHSSE---
                                                                 RNATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLL
                                                                                            LIADLTREKENLRRMVDAELDNVNKLKQEIEVTQESLENSRSEVSDITVQLEQLRDLSSK
                                                                                                                                                                                                                                                                                                   s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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filament-like protein 1.
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RESULT 37

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InterPro: IPR001609;
Pfam; PF00612; TQ; 1.
Pfam; PF00063; Myosin,
Pfam; PF02736; Myosin,
Pfam; PF01576; Myosin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-FEB-1996 (Rel. 33, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Myosin heavy chain, smooth muscle isof
                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92073350; PubMed-1961735;
Babij P., Kelly C., Periasamy M.;
"Characterization of a mammalian smooth muscle myosin heavy-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Choruaca; Chantaca, Chantaca, Chantaca, Cantaca, Chorudae; Mammalia; Eutheria; Lagomorpha; Leporidae;
                                                                                                                                             InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                           HSSP; P08799;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
ALKYLANED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2),
SUBCELLULAR LOCATION: Thick filements of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e: complete nucleotide and protein coding sequen 5. end of the gene."; c. Natl. Acad. Sci. U.S.A. 88:10676-10680(1991). FUNCTION: MUSCLE CONTRACTION.
                                                                                                                                                                                                                                                                                                    , M77812; AAA31395.1;
A41604; A41604.
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                                                                                                                                                                                                                                                                                                                                                                                             s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                            IPR000048; IQ
myosin_head;
Myosin_N; 1.
Myosin_tail;
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                                                                                                                    myosin_head.
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Best Local
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
MAR binding filament-like protein 1.
MFP1 OR AT3G15000 OR MSL1.4.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosida
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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               DNA Res. 7:131-135(2000).

-!- FUNCTION: BINDS DNA. INTERACTS WITH CHROMATIN VIA MATRIX
ATTACHMENT REGIONS (MARS). LIKELY TO PARTICIPATE IN NUCLEAR
ARCHITECTURE BY CONNECTING CHROMATIN WITH THE NUCLEAR MATRI)
                                                                                                                 STRAIN=CV. Columbia;
MEDLINE=20277480; PubMed=10819329;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata
"Structural analysis of Arabidopsis thaliana chromosome 3. I.
features of the regions of 4,504,864 bp covered by sixty Pl an
clones.";
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Calmodulin binding; ATP-binding; Methylation; Alkylation;
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ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
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P02566;
21-JUL-1986 (Rel. 01, 0
21-JUL-1986 (Rel. 01, 1
16-OCT-2001 (Rel. 40, 1
14-OCT-401 Reavy chain B (N
UNC-54 OR MYO-4.
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          SEQUENCE FROM N.A.
MEDLINE-83273600; PubMed-65;
Karn J., Brenner S., Barnett
"Protein structural domains
                                                                       Eukaryota; Metazoa;
Rhabditidae; Pelodes
                                                                                           Caenorhabditis elegans
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                              PubMed=6576334;
domains in the Caenorhabditis elegans gene are not separated by introns.";
                                                                       Nematoda; Chromadorea; cinae; Caenorhabditis.
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20.6%;
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McLachlan A.D., Karn J.;
"Periodic charge distributions in the
"Periodic charge distributions in muscle
                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00063; myosin_head; 1.
pfam; PF02736; Myosin_N; 1.
pfam; PF01576; Myosin_tall; 1.
prints; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The genes sup-7 x and sup-5 I nonsense mutations via altered Cell 33:575-583(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           match cross-bridge spacings Nature 299:226-231(1982).
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ATP-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 850-1966 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAR PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASES ACTIVITY.
MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN (CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBERRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY C.ELEGANS.
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SM00242; MYSc;
                                                                                                                                                                                                                                                                                                                     Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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; PubMed=6571695;
and R.F., Karn J.,
                     1880
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PubMed=7202124;
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Myosin_tail
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               ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (TRI-) (
METHYLATION (SH-1).
ALKYLATION (SH-2).
E -> R (IN REF. 2).
I -> L (IN REF. 2).
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ed transfer RNA.";
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COILED COIL (POTENTIAL)
ALPHA-HELICAL TAILPIECE
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Best Local Similarity
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Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eukaryota; Metazoa; Neoqnathae; Galliformes; Phasian
J.
[4]
           MEDLINE=88032919; PubMed=3312184; Maita T., Onishi H., Yajima E., Matsuda G.; "Amino acid sequence of the amino-terminal heavy chain of chicken gizzard myosin."; J. Blochem. 102:133-145(1987).
                                                                                                                                                 "Complete primary structure of vertebrate smooth muscle myosin chain deduced from its complementary DNA sequence. Implications topography and function of myosin.";
J. Mol. Biol. 198:143-157(1987).
                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-88118918; PubMed-2892941;
Yanagisawa M., Hamada Y., Katsura
                                                                                                                                                                                                                                                                                                                                       01-JUL-1989 (Rel. 11, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                         SEQUENCE OF 1-203.
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                                                                                                                Masaki T.;
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                                                                                                                                                                                                                                                                                                                            Myosin heavy chain, gizzard smooth muscle.
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01-JUL-1989
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pfam; PF01576; Myosin_tail; 1
prINTS; PR00193; MYOSINHEAVY
PrODom; PD000355; myosin_heac
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InterPro; IPR002928; Myosin_tail.
InterPro; IPR002017; Spectrin.
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use by non-profit institutions as long as its content
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Cell 94:559-571(1998)
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    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires
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HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
PTW. TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
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SIMILARITY: CONT.
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    W.
ALKYLATION (SH-1).
ALKYLATION (SH-2).
MISSING (IN REF. 3).
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KM; B7B6C923E5273D93 CRC64;
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light chain: visualization
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